

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 23, 2003, 18:00:50 : Search time 25.7561 Seconds
(without alignments)
1149.607 Million cell updates/sec

Title: US-10-088-548-2

Perfect score: 1786

Sequence: 1 KSPVVDQCHYDGRSYRIS.....YTMNPKLPDPCPLCASS 308

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :
1: PIR_73:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|----------|---|
| 1 | 1780 | 99.7 | 4548 | 1 S00657 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 2 | 1210.5 | 67.8 | 810 | 1 PIRHU | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 3 | 1205.5 | 67.5 | 810 | 2 B30848 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 4 | 1195.5 | 66.9 | 1420 | 2 A32869 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 5 | 1137.5 | 63.7 | 812 | 1 PLMS | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 6 | 1124 | 62.9 | 790 | 1 PLUG | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 7 | 1123.5 | 62.9 | 812 | 1 PLUG | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 8 | 1072 | 60.0 | 810 | 2 B61545 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 9 | 808.5 | 45.3 | 460 | 2 B61545 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 10 | 796 | 44.6 | 2869 | 2 T18518 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 11 | 787.5 | 44.1 | 455 | 2 A61545 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 12 | 685.5 | 38.4 | 728 | 2 A35644 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 13 | 685.5 | 38.4 | 728 | 2 A60185 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 14 | 680.5 | 38.1 | 728 | 1 JH0579 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 15 | 671 | 37.6 | 711 | 1 A47136 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 16 | 670.5 | 37.5 | 716 | 1 U5061 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 17 | 656 | 36.7 | 710 | 1 I51283 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 18 | 650.5 | 36.4 | 716 | 1 A40332 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 19 | 620 | 34.7 | 169 | 2 A40522 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 20 | 604.5 | 33.8 | 411 | 2 I51285 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 21 | 413 | 23.1 | 120 | 2 B61545 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 22 | 408 | 22.8 | 123 | 2 C61545 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 23 | 390 | 21.8 | 336 | 2 S3879 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 24 | 387 | 21.7 | 622 | 2 TBHU | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 25 | 363.5 | 20.4 | 625 | 2 TBBO | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 26 | 354 | 19.8 | 89 | 2 A60140 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 27 | 352.5 | 19.7 | 618 | 2 A35827 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 28 | 338.5 | 19.0 | 617 | 2 S10511 | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |
| 29 | 338 | 18.9 | 562 | 1 UKHUT | apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human |

ALIGNMENTS

RESULT 1
S00657
apolipoprotein(a) (EC 3.4.21.1) precursor [validated] - human
N:Alternate names: apolipoprotein(a); lipoprotein(a) chain apo(a)
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 08-Dec-2000
C:Accession: S00657; A28017; A47277; I60906; A47233; I52415; I65286
R:McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Nature 330, 132-137, 1987
A:Title: CDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
A:Reference number: S00657; M01D:88039109; PMID:3670400
A:Accession: S00657
A:Molecule type: mRNA
A:Residues: 1-4548 <MCL>
A:Cross-references: GB:X06696; EMBL:X06696; NID:928619; PIDN:CAA29618.1; PID:928620
R:Eaton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lam, Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
A:Title: Partial amino acid sequence of apolipoprotein(a) shows that it is homologous to plasminogen.
A:Reference number: A28017; M01D:87204109; PMID:3472206
A:Accession: A28017
A:Molecule type: protein
A:Residues: 20-21, 'P', '23-34', '17-179', 'N', '181-186', 'T', '188-196', 'DKG', '200-292-314', 'W', '31 X', '4396-4401 <EAT>
R:McLean, J.W.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz Proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993
A:Title: 5' control regions of the apolipoprotein(a) gene and members of the related A:Reference number: A47277; M01D:93165698; PMID:7679504
A:Accession: A47277
A:Molecule type: DNA
A:Status: preliminary; translation not shown; translated from GB/EMBL/DBJ
A:Residues: 1-16 <RES>
R:McGraw, R.; Maggioni, N.; Acquati, F.; Magnaghi, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; S Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A:Title: Characterization by yeast artificial chromosome cloning of the linked apoli A:Reference number: A47233; M01D:93087573; PMID:1454851
A:Accession: I60906
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RE2>
A:Cross-references: GB:M90078; NID:9178786; PIDN:AAA35547.1; PID:9553188
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: A47233
A:Molecule type: translation not shown; translated from GB/EMBL/DBJ
A:Residues: 1-16 <RE5>
R:Chen, E.Y.; Fless, G.M.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Biochemistry 31, 3113-3118, 1992
A:Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associate A:Reference number: I52415; M01D:92207924; PMID:1554698
A:Accession: I52415

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RB3>
A:Cross-references: GB:M86877; NID:q178780; PIDN:AAA6909.1; PID:9553185
A:Note: apo(a) gene 1 (nomenclature of reference I52415)
A:Accession: 165286
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <RB4>
A:Cross-references: GB:M86878; NID:q178782; PIDN:AAA51749.1; PID:9553186
C:Genetics:
A:Gene: GDB:LPA
A:Cross-references: GDB:120699; OMIM:152200
A:Map position: 6q26-6q27
A:Note: several genes closely linked on chromosome 6 are identical in the first coding
rs of kringle repeats
C:Superfamily: apolipoprotein(a); kringle homology; trypsin homology
C:Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
F:1-19/Domain: signal sequence #status predicted <SIC>
F:20-45/Domain: apolipoprotein(a) #status experimental <MAT>
F:28-105/Domain: kringle homology <KR1>
F:142-219/Domain: kringle homology <KR2>
F:256-333/Domain: kringle homology <KR3>
F:370-447/Domain: kringle homology <KR4>
F:484-561/Domain: kringle homology <KR5>
F:598-675/Domain: kringle homology <KR6>
F:712-789/Domain: kringle homology <KR7>
F:826-903/Domain: kringle homology <KR8>
F:940-1017/Domain: kringle homology <KR9>
F:1054-1131/Domain: kringle homology <KR10>
F:1168-1245/Domain: kringle homology <KR11>
F:1282-1359/Domain: kringle homology <KR12>
F:1396-1473/Domain: kringle homology <KR13>
F:1510-1587/Domain: kringle homology <KR14>
F:1624-1701/Domain: kringle homology <KR15>
F:1738-1815/Domain: kringle homology <KR16>
F:1852-1929/Domain: kringle homology <KR17>
F:1966-2043/Domain: kringle homology <KR18>
F:2080-2157/Domain: kringle homology <KR19>
F:2194-2271/Domain: kringle homology <KR20>
F:2308-2385/Domain: kringle homology <KR21>
F:2422-2499/Domain: kringle homology <KR22>
F:2536-2613/Domain: kringle homology <KR23>
F:2650-2727/Domain: kringle homology <KR24>
F:2764-2841/Domain: kringle homology <KR25>
F:2878-2955/Domain: kringle homology <KR26>
F:2992-3069/Domain: kringle homology <KR27>
F:3106-3183/Domain: kringle homology <KR28>
F:3220-3297/Domain: kringle homology <KR29>
F:3334-3411/Domain: kringle homology <KR30>
F:3448-3525/Domain: kringle homology <KR31>
F:3562-3639/Domain: kringle homology <KR32>
F:3676-3753/Domain: kringle homology <KR33>
F:3782-3859/Domain: kringle homology <KR34>
F:3896-3973/Domain: kringle homology <KR35>
F:4010-4087/Domain: kringle homology <KR36>
F:4124-4201/Domain: kringle homology <KR37>
F:4228-4307/Domain: kringle homology <KR38>
F:4328-4541/Domain: trypsin homology <TRY>

Query Match 99.7%; Score 1780; DB 1; Length 4548;
Best Local Similarity 99.7%; Pred. No. 2, 6e-123;
Matches 307; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
IV36

1 1 KSPVDDCYHGDGRSYRGISSTVTGRTGOSMSMTPHMHORPEYKPAAGLTENYCRNP 60
DB 4003 KSPVDDCYHGDGRSYRGISSTVTGRTGOSMSMTPHMHORPEYKPAAGLTENYCRNP 4062
61 DSKGQPCWCTTDFCVMEYCNLTQCESTESGVLEPTVVPVPSMEASHAAPTETQTPVVR 120
63 DSKGQPCWCTTDFCVMEYCNLTQCESTESGVLEPTVVPVPSMEASHAAPTETQTPVVR 4122
*HNGGQSGVRCGFSTTVIGRTGOSMSMTPHMHORPEYKPAAGLTENYCRNPADTGP 180

1V37

DB 4123 OCYHNGGQSGVRCGFSTTVIGRTGOSMSMTPHMHORPEYKPAAGLTENYCRNPADTGP 4182
QY 181 WCFITDPSIRMEYCNLTQCESTEGVAPPVVIOVPSIGPSEDDCFGNKGRKAT 240
DB 4183 WCFITDPSIRMEYCNLTQCESTEGVAPPVVIOVPSIGPSEDDCFGNKGRKAT 4242
QY 241 TVTGTGCEMAAOEHRHSTFIPGTNKAAGLEKNCRNPDDINGDMPCCYTNNPKRLDYC 300
DB 4243 TVTGTGCEMAAOEHRHSTFIPGTNKAAGLEKNCRNPDDINGDMPCCYTNNPKRLDYC 4302
QY 301 DIPICASS 308
DB 4303 DIPICASS 4310
V38

RESULT 2
pHUT
plasmin (EC 3.4.21.7) precursor [validated] - human
N:Alternate names: plasminogen precursor [misnomer]
N:Contains: angiotatin; microplasmin; plasminogen
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text change 15-Sep-2000
C:Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625;
R:Peterson, T.E.; Matzen, M.R.; Ichinose, A.; Davie, E.W.
J: Biol. Chem. 265, 6104-6111, 1990
A:Title: Characterization of the gene for human plasminogen, a key proenzyme in the f
A:Reference number: A35229; MUID:90202879; PMID:2318848
A:Accession: A35229
A:Molecule type: DNA
A:Residues: 1-810 <PER>
A:Cross-references: GB:J05286; GB:M34276; NID:q190064; PIDN:AAA60113.1; PID:9387026
A:Experimental source: leukocyte; lung fibroblast
R:Margaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.;
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A:Title: Definition of the transcription initiation site of human plasminogen gene in
A:Reference number: I52242; MUID:1095523; PMID:2268308
A:Accession: I52242
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-16 <MAL1>
A:Cross-references: GB:M62890; NID:q190092; PIDN:AAA34654.1; PID:9553613
R:Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A:Title: Molecular cloning and characterization of a full-length cDNA clone for human
A:Reference number: A26646; MUID:87162490; PMID:3030813
A:Accession: A26646
A:Molecule type: mRNA
A:Residues: 1-471, 'D', 473-810 <FOR>
A:Cross-references: GB:X05199; NID:q35530; PIDN:CAA28831.1; PID:935531
A:Experimental source: liver
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A:Title: Characterization of a complementary deoxyribonucleic acid coding for human a
A:Reference number: I45961; MUID:85023311; PMID:6148961
A:Accession: I45961
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 292-471, 'D', 473-810 <MAL2>
A:Cross-references: GB:K02922; NID:q190112; PIDN:AAA60124.1; PID:9387031.
A:Accession: I84609
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 367-419 <MAL3>
A:Cross-references: GB:K02921; NID:q190110; PIDN:AAA60123.1; PID:9190111
R:Brundholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergler, W.; Manneberg,
Eur. J. Biochem. 114, 465-470, 1981
A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of huma
A:Reference number: S03735; MUID:81212097; PMID:7238497
A:Accession: S03735
A:Molecule type: protein
A:Residues: 20-71, 'E', 73-76 <BRU>
R:Sottirup-Jensen, L.; Petersen, T.E.; Magnusson, S.